

SEQUENCE SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 03:18:06 ; Search time 8804 Seconds
 (without alignments)
 11070.431 Million cell updates/sec

Title: US-10-089-514-1
 Perfect score: 2061
 Sequence: 1 atgcgcacgcttctgatcga.....ccgtggcgggcgcggatga 2061
 Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0
 Searched: 4526729 seqs, 23644849745 residues
 Total number of hits satisfying chosen parameters: 9053458
 Minimum DB seq length: 0
 Maximum DB seq length: 20000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2061	100.0	2061	6	BD178313	GenBank — BD178313 Transform
2	2061	100.0	2061	6	BD093914	" — BD093914 Transform
3	2061	100.0	5251	1	AB116234	" — AB116234 Streptomy
4	1773.8	86.1	2660	1	SVU21728	GenBank — U21728 Streptomyce
5	1773.8	86.1	14159	1	AF262220	AF262220 Streptomy
6	820	39.8	2220	6	AR198361	AR198361 Sequence
7	820	39.8	4740	1	SPU60417	U60417 Streptomyce
8	773.4	37.5	4607	1	STMPABA	M93058 Streptomyce
9	773	37.5	39314	1	SGR300302	AJ300302 Streptomy
10	769.8	37.4	138203	1	AY310323	AY310323 Streptomy

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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 03:16:03 ; Search time 1005 Seconds
(without alignments)
10765.231 Million cell updates/sec

Title: US-10-089-514-1
Perfect score: 2061
Sequence: 1 atgcgcacgcttctgatcga.....ccgtggcggcgcccgatga 2061

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB	
1	2061	100.0	2061	4	AAF86409	W0 01/23542 Aaf86409 4-amino-4
2	2061	100.0	2061	8	AAL50180	W0 02/77244 Aal50180 S venezue
3	1773.8	86.1	3305	8	ABZ69799	Abz69799 Plasmid p
4	1772.2	86.0	12391	8	ABZ69798	Abz69798 Plasmid p
5	459	22.3	4496	2	AAT58553	Aat58553 Streptomy

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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 04:42:01 ; Search time 181 Seconds
(without alignments)
8093.568 Million cell updates/sec

Title: US-10-089-514-1
Perfect score: 2061
Sequence: 1 atgcgcacgcttctgatcga.....ccgtggcgggcgcggatga 2061

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
ID						
1	820	39.8	2220	3	US-08-765-907A-14	Sequence 14, Appl
2	459	22.3	4496	3	US-08-765-907A-6	Sequence 6, Appli
3	365.4	17.7	2888	3	US-08-765-907A-1	Sequence 1, Appli
4	272.2	13.2	645	2	US-08-403-852D-9	Sequence 9, Appli
5	272.2	13.2	645	3	US-08-510-646B-9	Sequence 9, Appli
6	272.2	13.2	645	3	US-09-231-818-9	Sequence 9, Appli
7	272.2	13.2	645	4	US-09-635-359B-9	Sequence 9, Appli
c	8	268.4	13.0	1101	4	US-09-252-991A-13413
	9	268.4	13.0	1431	4	US-09-252-991A-13733
	10	260	12.6	816	4	US-09-252-991A-13943
	11	197.8	9.6	1506	4	US-09-252-991A-811

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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 04:52:43 ; Search time 1044 Seconds
(without alignments)
10667.498 Million cell updates/sec

Title: US-10-089-514-1
Perfect score: 2061
Sequence: 1 atgcgcacgcttctgatcga.....ccgtggcgggcgcggatga 2061

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 7255776

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PECTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

instant application NOT published

Result	Query						Description
No.	Score	Match	Length	DB	ID		
1	2061	100.0	2061	18	US-10-472-587-1	✓	Sequence 1, Appli
2	1773.8	86.1	3305	14	US-10-126-927-68		Sequence 68, Appli
3	1772.2	86.0	12391	14	US-10-126-927-67		Sequence 67, Appli
4	606.2	29.4	2196	15	US-10-156-761-1167		Sequence 1167, Appli
c 5	606.2	29.4	9025608	15	US-10-156-761-1		Sequence 1, Appli
6	301.4	14.6	9025608	15	US-10-156-761-1		Sequence 1, Appli
7	280.8	13.6	1479	15	US-10-156-761-6148		Sequence 6148, Appli
8	270	13.1	1362	16	US-10-282-122A-30135		Sequence 30135, Appli
9	266.8	12.9	1860	9	US-09-738-626-1111		Sequence 1111, Appli
10	266.8	12.9	3309400	9	US-09-738-626-1		Sequence 1, Appli
c 11	234.8	11.4	42000	17	US-10-159-257A-1		Sequence 1, Appli
c 12	234.8	11.4	63158	15	US-10-292-198-1		Sequence 1, Appli
13	231.6	11.2	1338	16	US-10-282-122A-32104		Sequence 32104, Appli
14	224.2	10.9	2523	16	US-10-282-122A-17825		Sequence 17825, Appli
15	220.4	10.7	1257	16	US-10-282-122A-33856		Sequence 33856, Appli
16	210.2	10.2	2160	14	US-10-138-927-76		Sequence 76, Appli
17	210.2	10.2	2160	14	US-10-138-927-83		Sequence 83, Appli
18	210.2	10.2	2160	15	US-10-430-011-76		Sequence 76, Appli
19	210.2	10.2	2160	15	US-10-430-011-83		Sequence 83, Appli
20	210.2	10.2	2160	15	US-10-430-011-126		Sequence 126, Appli
21	201.2	9.8	2199	15	US-10-430-011-122		Sequence 122, Appli
22	198.2	9.6	1353	16	US-10-282-122A-23903		Sequence 23903, Appli
23	196.4	9.5	636	15	US-10-156-761-4319		Sequence 4319, Appli
24	192.8	9.4	2256646	17	US-10-470-565-1		Sequence 1, Appli
25	190.4	9.2	1323	16	US-10-282-122A-19610		Sequence 19610, Appli
26	189.6	9.2	2190	14	US-10-138-927-75		Sequence 75, Appli
27	189.6	9.2	2190	15	US-10-430-011-75		Sequence 75, Appli
28	186	9.0	661	18	US-10-425-115-81629		Sequence 81629, Appli
29	182.2	8.8	2166	15	US-10-430-011-127		Sequence 127, Appli
30	180.8	8.8	2202	15	US-10-430-011-121		Sequence 121, Appli
31	178.6	8.7	65140	17	US-10-203-295-1		Sequence 1, Appli
32	178.6	8.7	125401	17	US-10-203-295-35		Sequence 35, Appli
33	173.8	8.4	2190	14	US-10-138-927-93		Sequence 93, Appli
34	173.8	8.4	2190	15	US-10-430-011-93		Sequence 93, Appli
35	173.6	8.4	1119	15	US-10-156-761-6781		Sequence 6781, Appli
36	170.6	8.3	2190	14	US-10-138-927-1		Sequence 1, Appli
37	170.6	8.3	2190	14	US-10-138-927-84		Sequence 84, Appli
38	170.6	8.3	2190	14	US-10-138-927-85		Sequence 85, Appli
39	170.6	8.3	2190	14	US-10-138-927-86		Sequence 86, Appli
40	170.6	8.3	2190	14	US-10-138-927-87		Sequence 87, Appli
41	170.6	8.3	2190	14	US-10-138-927-88		Sequence 88, Appli
42	170.6	8.3	2190	14	US-10-138-927-92		Sequence 92, Appli
43	170.6	8.3	2190	15	US-10-430-011-1		Sequence 1, Appli
44	170.6	8.3	2190	15	US-10-430-011-84		Sequence 84, Appli
45	170.6	8.3	2190	15	US-10-430-011-85		Sequence 85, Appli

ALIGNMENTS

RESULT 1

US-10-472-587-1

; Sequence 1, Application US/10472587

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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 04:40:31 ; Search time 6560 Seconds
(without alignments)
11448.519 Million cell updates/sec

Title: US-10-089-514-1

Perfect score: 2061

Sequence: 1 atgcgcacgcttctgatcga.....ccgtggcgggccccatga 2061

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	216.6	10.5	529	6	CA003778	CA003778 HS15I14r
2	212.8	10.3	845	8	BZ570522	BZ570522 msh2_1411
3	205.8	10.0	653	7	CF863831	CF863831 psZS008xG
4	195.6	9.5	1043	8	BZ548859	BZ548859 pacsl-60
c 5	178	8.6	523	8	BZ412600	BZ412600 OGAAG11TM
6	178	8.6	631	8	BZ412593	BZ412593 OGAAG11TC
7	178	8.6	631	8	BZ537360	BZ537360 OGAGD95TC
c 8	178	8.6	810	9	CG170785	CG170785 PUIIR58TD